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RL J. BIOL. CHEM. 267:21172-21178(1992).
CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNF-ALPHA AND
CC APPROXIMATELY 3-FOLD LOWER AFFINITY FOR TNF-BETA.
CC -1- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW
CC LEVEL ON THREONINE RESIDUES.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL; M35857; G339752; -.
DR EMBL; M35857; G339752; -.
DR EMBL; M53954; G339758; -.
DR PIR; A35356; A35356.
DR PIR; A36007; A36007.
DR PIR; A36475; A36475.
DR PIR; B35010; B35010.
DR PIR; A23666; A23666.
DR HSSP; P19438; 1TNR.
DR MIM; 191191; -.
DR PROSITE; PS00652; TNFR_NGFR.
DR RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL.
KW PHOSPHORYLATION.
FT SIGNAL 1 22
FT CHAIN 23 461 TUMOR NECROSIS FACTOR RECEPTOR 2.
FT DOMAIN 23 257 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 288 461 POTENTIAL.
FT DOMAIN 288 461 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 39 201 4 X TNFR-CYS.
FT REPEAT 39 76 TNFR-CYS 1.
FT REPEAT 77 118 TNFR-CYS 2.
FT REPEAT 119 162 TNFR-CYS 3.
FT REPEAT 163 201 TNFR-CYS 4.
FT DISULFID 40 53 BY SIMILARITY.
FT DISULFID 54 67 BY SIMILARITY.
FT DISULFID 57 75 BY SIMILARITY.
FT DISULFID 78 93 BY SIMILARITY.
FT DISULFID 96 110 BY SIMILARITY.
FT DISULFID 100 118 BY SIMILARITY.
FT DISULFID 120 126 BY SIMILARITY.
FT DISULFID 134 143 BY SIMILARITY.
FT DISULFID 137 161 BY SIMILARITY.
FT DISULFID 164 179 BY SIMILARITY.
FT DISULFID 171 171 POTENTIAL.
FT CARBOHYD 193 193 POTENTIAL.
FT CARBOHYD 141 141 R -> P (IN REF. 3).
FT CONFLICT 196 196 R -> T (IN REF. 1).
FT CONFLICT 363 363 A -> T (IN REF. 3).
SQ SEQUENCE 461 AA; 48316 MW; 0F5D0C44 CRC32;
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Query Match 13.4%; Score 405; DB 9; Length 461;
Best Local Similarity 41.8%; Pred. No. 1,33e-63;
Matches 69; Conservative 26; Mismatches 59; Indels 11; Gaps 8;
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Db 45 yydqta-gmccskcspgqahkvcfctktsdtycdscdsdytlmwnvpcjlsgrcsad 103
| : : : : : | : : : : : | : : : : : | : : : : : |
Oy 31 YDEFTSHQLDKCPFGYLLKQHCYAKWTCVPCPDHYTDSMHTSDCLYCSPVKEL 90
| : : : : : | : : : : : | : : : : : | : : : : : |
Db 104 qyctactcagrrictcrprycaiskgqgcicaplrcrpgfyavarpqtsdvckp 163
| : : : : : | : : : : : | : : : : : | : : : : : |
Oy 91 QYVKQECNTHNRVCEKGRY--LEI-EFC-L-RH-RSCPFGFVQAGTPERNVCKR 144
| : : : : : | : : : : : | : : : : : | : : : : : |
Db 164 cagpfntstsdicrphqicnvaia--p-gnasrdvcsts 204
| : : : : : | : : : : : | : : : : : | : : : : : |
Oy 145 CPDGFSTNETSSKAPCRKHTNCSVFGLLTQKGNATHDNCSGNS 189
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RESULT 2
ID TNR2.MOUSE STANDARD: PRT: 474 AA.
AC P25119;
DT 01-MAY-1992 (REL. 22, CREATED)
DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TNF-R2) (P75).
GN TNFR2 OR TNFR-2.
OS MUS MUSCULUS (MOUSE).
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OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE; 91187885.
RA LEWIS M., TARTAGLIA L.A., LEE A., BENNETT G.L., RICE G.C.,
RA WONG G.H., CHEN E.Y., GOEDEL D.V.;
RL PROC. NATL. ACAD. SCI. U.S.A. 88:2830-2834(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91246168.
RA GOODWIN R.G., ANDERSON D., JERZY R., DAVIS T., BRANNAN C.I.,
RA COPELAND N.G., JENKINS N.A., SMITH C.A.;
RL MOL. CELL. BIOL. 11:3020-3026(1991).
CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL; M60469; G199828; -.
DR EMBL; M59378; G202095; -.
DR PIR; B38634; B38634.
DR HSSP; P19438; 1TNR.
DR PROSITE; PS00652; TNFR_NGFR.
DR RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL.
KW PHOSPHORYLATION.
FT SIGNAL 1 22
FT CHAIN 23 474 TUMOR NECROSIS FACTOR RECEPTOR 2.
FT DOMAIN 23 258 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 259 288 POTENTIAL.
FT DOMAIN 289 474 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 39 203 4 X TNFR-CYS.
FT REPEAT 39 77 TNFR-CYS 1.
FT REPEAT 78 119 TNFR-CYS 2.
FT REPEAT 120 164 TNFR-CYS 3.
FT REPEAT 165 203 TNFR-CYS 4.
FT DISULFID 40 54 BY SIMILARITY.
FT DISULFID 55 68 BY SIMILARITY.
FT DISULFID 58 76 BY SIMILARITY.
FT DISULFID 79 94 BY SIMILARITY.
FT DISULFID 97 111 BY SIMILARITY.
FT DISULFID 101 119 BY SIMILARITY.
FT DISULFID 121 127 BY SIMILARITY.
FT DISULFID 136 145 BY SIMILARITY.
FT DISULFID 139 163 BY SIMILARITY.
FT DISULFID 166 181 BY SIMILARITY.
FT CARBOHYD 69 69 POTENTIAL.
FT CARBOHYD 195 195 POTENTIAL.
SQ SEQUENCE 474 AA; 50319 MW; DC32B2B6 CRC32;
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Query Match 12.4%; Score 375; DB 9; Length 474;
Best Local Similarity 41.5%; Pred. No. 9.05e-57;
Matches 66; Conservative 21; Mismatches 61; Indels 11; Gaps 7;
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Db 52 gmcackcprggyvnhfcmktsdtycadcaeamyqtqvnqfctlsccsctdqvclrac 111
| : : : : : | : : : : : | : : : : : | : : : : : |
Oy 38 QLLDCKCPFGYLLKQHCYAKWTCVPCPDHYTDSMHTSDCLYCSPVKELQYKQEC 97
| : : : : : | : : : : : | : : : : : | : : : : : |
Db 112 tkqgnryvacaagaycaalkthsgscrgcmrlskcprgfyavassarpgnvlckacagtf 171
| : : : : : | : : : : : | : : : : : | : : : : : |
Oy 98 NRTNHRVCEKGRY--LEIEF--CLKH-R-S-CPDGFVQAGTPERNVCKRCPDGF 150
| : : : : : | : : : : : | : : : : : | : : : : : |
Db 172 sdtstsdicrphicst--laip--gnastdaycapes 206
| : : : : : | : : : : : | : : : : : | : : : : : |
Oy 151 SNETSSKAPCRKHTNCSVFGLLTQKGNATHDNCSGNS 189
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RESULT 3
ID CD40.HUMAN STANDARD: PRT: 277 AA.
AC P25942;
DT 01-MAY-1992 (REL. 22, CREATED)
DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).
GN CD40.
OS HOMO SAPIENS (HUMAN).
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OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE: 89356608.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 RL EMO J. 8:1403-1410(1989).
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CAECINOMAS.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL: X60592; G29851; -.
 DR PIR: S04460; S04460.
 DR MIM: 109535; -.
 DR PROSITE: PS00652; TNFR_NGFR.
 KW RECEPTOR; B-CELL; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 277
 FT DOMAIN 20 193
 FT TRANSMEM 194 215
 FT DOMAIN 216 277
 FT DOMAIN 25 187
 FT REPEAT 25 60
 FT REPEAT 61 103
 FT REPEAT 104 144
 FT REPEAT 145 187
 FT CARBOHYD 153 180
 FT SEQUENCE 277 AA; 30619 MW; 38284411 CRC32;
 Query Match 10.0%; Score 303; DB 2; Length 277;
 Best Local Similarity 36.8%; Pred. No. 1.03e-40;
 Matches 56; Conservative 21; Mismatches 67; Indels 8; Gaps 7;
 Db 38 cdlcpgsgqtlvscdtefeetecelcpesefldtmrcthchkycdpn-iglr-vqgkq 95
 Qy 41 CDKCPGTYLKHCHTAKMTVCAPCPDHYYTDSWHTSDCC-L--YCSYCKELQYVKQEC 97
 Db 96 tsecltctceegwhntseacescvlhrscspgfygkqlatgvsdlcpcpvgffnvs 155
 Qy 98 NRTNHRVCECKEGRY-L-EI-EFCLKHSRCPGFGVQAGTPERTVCKRCPDGFFSNET 154
 Db 156 safekchpwtscetkdlvvgagatnktvvcg 187
 Qy 155 SSKAPCRKHTNCSVGLLTOKGNATHDNICS 186
 RESULT 4
 AC CD40_MOUSE STANDARD: PRT; 289 AA.
 AC P27512;
 DT 01-AUG-1992 (REL. 23, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDM40).
 GN CD40.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE: 92105763.
 RA TORRES R.M., CLARK E.A.;
 RL J. IMMUNOL. 148:620-626(1992).
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL: M94126; G192526; -.
 DR EMBL: M94126; G192526; JOINED.
 DR EMBL: M94128; G192526; JOINED.
 DR EMBL: M94127; G192526; JOINED.
 DR PIR: A46476; A46476.
 DR HSSP: P19438; TNFR.
 DR PROSITE: PS00652; TNFR_NGFR.
 KW RECEPTOR; B-CELL; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 289
 FT DOMAIN 20 193
 FT TRANSMEM 194 215
 FT DOMAIN 216 289
 FT DOMAIN 25 187
 FT REPEAT 25 60
 FT REPEAT 61 103
 FT REPEAT 104 144
 FT REPEAT 145 187
 FT CARBOHYD 153 153
 FT SEQUENCE 289 AA; 32111 MW; D8D70A2C CRC32;
 Query Match 9.7%; Score 294; DB 2; Length 289;
 Best Local Similarity 38.8%; Pred. No. 9.50e-39;
 Matches 59; Conservative 20; Mismatches 65; Indels 8; Gaps 6;
 Db 38 cdlcpgsrltshctalcctqchpcdsgefsaqwnrelrcthchhcepn-qglr-vkheg 95
 Qy 41 CDKCPGTYLKHCHTAKMTVCAPCPDHYYTDSWHTSDCC-LY--CSYVCKELQYVKQEC 97
 Db 96 taesdtctctceegwhntseacescvlhrscspgfygkqlatgvsdlcpcpvgffnvs 155
 Qy 98 NRTNHRVCECKEGRY-L-EI-EFCLKHSRCPGFGVQAGTPERTVCKRCPDGFFSNET 154
 Db 156 slfekcypwtscetkdlvvgagatnktvvcg 187
 Qy 155 SSKAPCRKHTNCSVGLLTOKGNATHDNICS 186

RA HOWARD M., COCKAYNE D.A.;
 RL J. IMMUNOL. 149:3921-3926(1992).
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL: M83112; G1553059; -.
 DR EMBL: M94126; G192526; -.
 DR EMBL: M94126; G192526; JOINED.
 DR EMBL: M94128; G192526; JOINED.
 DR EMBL: M94127; G192526; JOINED.
 DR PIR: A46476; A46476.
 DR HSSP: P19438; TNFR.
 DR PROSITE: PS00652; TNFR_NGFR.
 KW RECEPTOR; B-CELL; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 289
 FT DOMAIN 20 193
 FT TRANSMEM 194 215
 FT DOMAIN 216 289
 FT DOMAIN 25 187
 FT REPEAT 25 60
 FT REPEAT 61 103
 FT REPEAT 104 144
 FT REPEAT 145 187
 FT CARBOHYD 153 153
 FT SEQUENCE 289 AA; 32111 MW; D8D70A2C CRC32;
 Query Match 9.7%; Score 294; DB 2; Length 289;
 Best Local Similarity 38.8%; Pred. No. 9.50e-39;
 Matches 59; Conservative 20; Mismatches 65; Indels 8; Gaps 6;
 Db 38 cdlcpgsrltshctalcctqchpcdsgefsaqwnrelrcthchhcepn-qglr-vkheg 95
 Qy 41 CDKCPGTYLKHCHTAKMTVCAPCPDHYYTDSWHTSDCC-LY--CSYVCKELQYVKQEC 97
 Db 96 taesdtctctceegwhntseacescvlhrscspgfygkqlatgvsdlcpcpvgffnvs 155
 Qy 98 NRTNHRVCECKEGRY-L-EI-EFCLKHSRCPGFGVQAGTPERTVCKRCPDGFFSNET 154
 Db 156 slfekcypwtscetkdlvvgagatnktvvcg 187
 Qy 155 SSKAPCRKHTNCSVGLLTOKGNATHDNICS 186
 RESULT 5
 ID VT2_MTXVL STANDARD: PRT; 326 AA.
 AC P29825;
 DT 01-APR-1993 (REL. 25, CREATED)
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
 DT 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
 DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
 GN T2.
 OS MYXOMA VIRUS (STRAIN LAUSANNE).
 OC VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXYIRIDAE; CHOROPOXYIRINAE;
 OC LEOPOROVIRUSES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE: 91335768.
 RA UPON C., MACEN J.L., SCHREIBER M., MCFADDEN G.;
 RL VIROLOGY 184:370-382(1991).
 CC -1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
 REACH CELLULAR TARGET AND THEREBY DEAMPEING THE POTENTIAL
 ANTI-VIRAL EFFECTS OF THE CYTOKINE.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL: M95181; G332310; -.
 DR EMBL: A23729; E199442; -.
 DR PIR: A40566; GOVZML.
 DR HSSP: P19438; TNFR.
 DR PROSITE: PS00652; TNFR_NGFR.
 KW RECEPTOR; GLYCOPROTEIN; REPEAT; SIGNAL.
 FT SIGNAL 1 16
 FT CHAIN 17 326
 FT DOMAIN 27 186

FT	DISULFID	104	124	BY SIMILARITY
FT	DISULFID	106	132	BY SIMILARITY.
FT	DISULFID	139	150	BY SIMILARITY.
FT	DISULFID	142	169	BY SIMILARITY.
FT	DISULFID	172	187	BY SIMILARITY.
FT	CARBOHYD	40	40	POTENTIAL.
FT	CARBOHYD	179	179	POTENTIAL.
SO	SEQUENCE	415 AA;	44956 MM; 3C5DD121 CRC32;	
Query Match				
Best Local Similarity		8.7%;	Score 265;	DB 9;
Matches		54;	Conservative	30;
			Mismatches	92;
			Indels	11;
			Gaps	
Db	52	epmhvccsircpbgfefavcsisqgdvctkctphnsnehmhlstcqlcrp-cdiylgf	111	g
QY	34	ETSHQLLDCKPCPGTYLKHCHTAKMKVCACPCPDHYTDSWHTSDCELYCSPWKE-LQY	92	
Db	111	eevapcsdrkhaercqpgmscvlldeochnceeerlvcqpgfreaevteindtdncv	170	
QY	93	VK-OECNTHNRVCEKEGR---YLEIE--FCLNHR-S-CPGCGV-VQAGTPERNIVCK	143	
Db	171	pckpghfngntsparcqphtrceigglveaapgtsydtcknkppegamllatllsl	230	
QY	144	RCPPGFESNENSSAKPCKRHNCVFGILLQKNAHNDHCNSNSTQKCGIDVTLCE	203	
Db	231	vllllftc 237		
QY	204	EAFFRFA 210		
RESULT 7				
ID	VT2_STVKA	STANDARD;	PRT;	325 AA.
AC	P25943;			
DT	01-MAY-1992 (REL. 22, CREATED)			
DT	01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)			
DT	01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)			
DE	TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).			
GN	T2.			
OS	SHOPE FIBROMA VIRUS (STRAIN KASZA) (SFV).			
OC	VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXYIRIDAE; CHORDOPOXVIRINAE;			
OC	LEPORIPVIRUSES.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 87321103.			
RA	UPTON C., DELANGE A.M., MCFADDEN G.;			
RN	VIROLOGY 160:20-30(1987).			
RP	[2]			
RP	FUNCTION.			
RX	MEDLINE; 91207415.			
RA	SMITH C.A., DAVIS T., WIGNALL J.M., DIN W.S., FARRAH T., UPTON C.,			
RA	MCFADDEN G., GOODMAN R.G.;			
RL	BIOCHEM. BIOPHYS. RES. COMMUN. 176:335-342(1991).			
CC	-1- FUNCTION. BINDS TO TNF-ALPHA AND BETA, PROBABLY PREVENTS TNF TO			
CC	RACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL			
CC	ANTIVIRAL EFFECTS OF THE CYTOKINE.			
CC	-1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.			
DR	EMBL; M17433; -, NOT ANNOTATED.CDS.			
DR	EMBL; A23727; E199408; -.			
DR	PIR; B43692; B43692.			
DR	HSP; P19438; 1TNF.			
DR	PROSITE; PS00652; TNFR_NGFR.			
KW	RECEPTOR; GLYCOPROTEIN; REPEAT; SIGNAL.			
FT	SIGNAL	1	16	POTENTIAL.
FT	CHAIN	17	325	PROTEIN T2.
FT	DOMAIN	27	186	4 X TNFR-CYS.
FT	REPEAT	27	62	TNFR-CYS 1.
FT	REPEAT	63	104	TNFR-CYS 2.
FT	REPEAT	105	147	TNFR-CYS 3.
FT	REPEAT	148	186	TNFR-CYS 4.
FT	CARBOHYD	105	105	POTENTIAL.
FT	CARBOHYD	181	181	POTENTIAL.
FT	CARBOHYD	205	205	POTENTIAL.
FT	CARBOHYD	238	238	POTENTIAL.

FT	CANBOHYD	177		177	POTENTIAL.
SQ	SEQUENCE	435 AA;	46709 MW;	203882DD CRC32;	
	Query Match		8.6%;	Score 260;	DB 91; Length 435;
	Best Local Similarity	32.3%;	Pred. No. 1.97e-31;		
	Matches	52;	Conservative	23;	Mismatches 75; Indels 11; Gaps 6;
Dd	52	epqhticsrcppgtylvaksosrlrdtcvcaetsnehnmylltclqlcrpcdpv-mgl 110			
Oy	34	ETSHQLCDKCRPPETYLKHQTAKMKRVACPCPDHYTDSMHTSDC-LY--CSFVKEL 90			
Dd	111	eelp-ctskrkktcqrqgmfcawalectheellisdcppteaelkdvxkgynhcvp 169			
Oy	91	QVVAOECKRTHNRACEKEGRY-----LEIEFLCHKHRSCEPFGGV-VQAQTPERNWCKR 144			
Dd	170	kaghtqntsparscqphltccngjveapagtadtcc 210			
Oy	145	CPDGFSNETSSKAPCRKHNCVSFGLLTQKGATHDNIC 185			
RESULT	9	STANDARD;	PRT;	349 AA.	
ID	VCC2 VARV				
AC	P34015;				
DT	01-FEB-1994 (REL. 28, CREATED)				
DT	01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)				
DT	01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)				
DE	PROTEIN C22/B28 HOMOLOG.				
GN	GAR.				
OS	VARIOLA VIRUS.				
OC	VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXYVIRIDAE; CHORDOPOXVIRINAE;				
OC	ORTHOPOXYVIRUSES.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-INDIA-1967 / ISOLATE INDJ;				
RX	MEDLINE; 93202281.				
RA	SHCHELKUNOV S.N., BLINOV V.M., SANDAKHCHEV L.S.;				
RL	FEB5 LETT. 319:80-83(1993).				
CC	-1- SMILAIRITY: CONTAINS TWO LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGIONS.				
DR	EMBL; X671177.GS16449; -.				
DR	PIR; D36858; D36858.				
DR	PIR; S35987; S35987.				
DR	PIR; S46888; S46888.				
DR	HSSP; P19438; 1TNF.				
DR	PROSITE; PS00652; TNFR_NGFR.				
KW	REPEAT.				
FT	DOMAIN	31	108	2 X TNFR-CYS.	
FT	REPEAT	31	66	TNFR-CYS 1.	
FT	REPEAT	67	108	TNFR-CYS 2.	
SQ	SEQUENCE	349 AA;	38189 MW;	50DOB435 CRC32;	
	Query Match		7.7%;	Score 233;	DB 10; Length 349;
	Best Local Similarity	32.0%;	Pred. No. 9.20e-26;		
	Matches	54;	Conservative	26;	Mismatches 79; Indels 10; Gaps 7;
Dd	1	mkslylylflfslcllngrdaapytpnkkckdeykrhmloclseppgtysirlcdsk 60			
Oy	1	MKKLLCALVLD-ISIKWTTOETFPFKYLHYDE-E-TSHQLCDKCRPPETYLKHQTAK 57			
Dd	61	tntqctocgsqstsrnmhlpaciscrgcnsmqvetscntlnricscspgyallkg 120			
Oy	58	WKTYCAPCPDHYYTDSMHTSECLCYSPCKEKLQYVAGCECNRRHNHRACEKEGRY--LE- 114			
Dd	121	ssgcacvsqtckgiygvsv-ghtsvadvicspcgfiglyshvtvsadkc 168			
Oy	115	-IE--FCILKHRSCEPFGGVVQAQTPERNWCKRCPDGFSNETSSKAPC 160			
RESULT	10	STANDARD;	PRT;	454 AA.	
ID	TNRL MOUSE				
AC	P25118;				
DT	01-MAY-1992 (REL. 22, CREATED)				
DT	01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)				

FT DISULFID 105 125 BY SIMILARITY.
FT DISULFID 127 143 BY SIMILARITY.
FT DISULFID 146 158 BY SIMILARITY.
FT DISULFID 149 166 BY SIMILARITY.
FT DISULFID 168 179 BY SIMILARITY.
FT DISULFID 182 191 BY SIMILARITY.
FT DISULFID 185 195 BY SIMILARITY.
FT CARBOHYD 54 54 POTENTIAL.
FT CARBOHYD 151 151 POTENTIAL.
FT CARBOHYD 201 201 POTENTIAL.
SQ SEQUENCE 461 AA; 50969 MW; 82F68B08 CRC32;

Query Match 7.3%; Score 220; DB 9; Length 461;
Best Local Similarity 33.8%; Pred. No. 4.35e-23;
Matches 49; Conservative 22; Mismatches 63; Indels 11; Gaps 10;

Db 49 yabphnslcctckhkylysdcpspgqetvcevdckgftlasqnhvrglscctcke 108
31 YDETSHOLLCDKCPGPTYLKQHCITAK-WKTVCAPCPDHYTDSMHTSDCLCSPVCKE 89
109 mfvvelspckadmdtvcgckngfylysethfgcvdscpfng-tvllpckekqnlvcn 167
90 L-OYVQKQECNRTNRYCECK--E-GRYL-EIEF-CLKHNSCPGFGVYQAGTEPRNTVCK 143
168 -chagfflsgnecpschckngcc 191
144 RCPDGF-S-NETSSKAPCKRHTNC 166

QY 144 RCPDGF-S-NETSSKAPCKRHTNC 166

RESULT 12
ID NGFR-CHICK STANDARD; PRT; 416 AA.
AC P18519;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
DE (GP80-LNGFR).
OS GALLUS GALLUS (CHICKEN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
OC GALLIFORMES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE: 90166579.
RA LARGE T.H., WESKAMP G., HELDER J.C., RADEKE M.J., MISKO T.P.,
RA SHOOTER E.M., REICHARDT L.F.;
RA NEURON 2:1123-1134(1989).
RL [2]
[2] SEQUENCE OF 21-416 FROM N.A.
MEDLINE: 90152140.
RA HEUER J.G., FATEME-NAINIE S., WHEELER E.F., BOTHWELL M.;
RA DEV. BIOL. 137:287-304(1990).
CC -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
CC NT-3, AND NT-4.
CC -1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
CC BOND FORMATION.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC PIR: J00006; J00504.
DR PIR: A60504; A60504.
DR PROSITE: PS00652; TNFR_NGFR.
DR PROSITE: PS00017; DEATH_DOMAIN.
DR RECEPTOR; NEUROGENESIS; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT;
KM PHOSPHORYLATION; SIGNAL.
FT CHAIN 1 19 POTENTIAL.
FT CHAIN 20 416 NGF RECEPTOR.
FT DOMAIN 29 239 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 240 261 POTENTIAL.
FT DOMAIN 262 416 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 23 181 4 X TNFR-CYS.
FT REPEAT 23 57 TNFR-CYS 1.
FT REPEAT 58 100 TNFR-CYS 2.

FT REPEAT 101 140 TNFR-CYS 3.
FT REPEAT 141 181 TNFR-CYS 4.
FT DOMAIN 188 236 SER/THR-RICH.
FT DOMAIN 333 410 DEATH DOMAIN.
FT DISULFID 24 35 BY SIMILARITY.
FT DISULFID 36 49 BY SIMILARITY.
FT DISULFID 39 56 BY SIMILARITY.
FT DISULFID 59 75 BY SIMILARITY.
FT DISULFID 78 91 BY SIMILARITY.
FT DISULFID 81 99 BY SIMILARITY.
FT DISULFID 101 114 BY SIMILARITY.
FT DISULFID 117 130 BY SIMILARITY.
FT DISULFID 120 138 BY SIMILARITY.
FT DISULFID 141 156 BY SIMILARITY.
FT DISULFID 159 172 BY SIMILARITY.
FT DISULFID 162 180 BY SIMILARITY.
FT CARBOHYD 52 52 POTENTIAL.
FT CARBOHYD 36 36 C->Y (IN REF. 2).
FT CONFLICT 173 173 T->K (IN REF. 2).
FT CONFLICT 276 276 N->S (IN REF. 2).
FT CONFLICT 396 396 K->R (IN REF. 2).
SQ SEQUENCE 416 AA; 44654 MW; 4D3F086A CRC32;

Query Match 7.1%; Score 215; DB 6; Length 416;
Best Local Similarity 30.4%; Pred. No. 4.53e-22;
Matches 45; Conservative 27; Mismatches 70; Indels 6; Gaps 6;

Db 36 ckaclnlgvvgpvcgvn-qtvcpcldsvtsdvatepckpctq-cvylhmsapcve 93
41 CDKCPGTYLKQHCITAKWMTVCAPCPDH-YTDSMHTSDCLCSPVCKELOYKQECNR 99
94 sddavrcaygyfdealspsckecscicevgfllmfcidsqdtvceecpeltfsdaantv 153
100 TNHRYCECKEGRYL-EIE-FCLKHNSCPGFGVYQAGTEPRNTVCKRCPDGFSSNETSSK 157
154 dplpcticeenwvmeke-ctatsdaec 180
158 APCRKHNTCSVFGLLTKGNATHDNIC 185

QY 158 APCRKHNTCSVFGLLTKGNATHDNIC 185

RESULT 13
ID NGFR-HUMAN STANDARD; PRT; 427 AA.
AC P08138;
DT 01-AUG-1988 (REL. 08, CREATED)
DT 01-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
DE (GP80-LNGFR).
OS NGFR.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 87051725.
RA JOHNSON D., LANAHAN A., BUCK C.R., SEHGAL A., MORGAN C., MERCER E.,
RA BOTHWELL M., CHAO M.;
RA CELL 47:545-554(1986).
RL -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
CC NT-3, AND NT-4.
CC -1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
CC BOND FORMATION.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC EMBL: M14764; G189205; -.
DR EMBL: A25218; G0H0N.
DR PIR: A25218; G0H0N.
DR HSSP: P19438; ITNR.
DR MIM: 162010; -.
DR PROSITE: PS00652; TNFR_NGFR.
DR PROSITE: PS00017; DEATH_DOMAIN.
DR RECEPTOR; NEUROGENESIS; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT;
KM PHOSPHORYLATION; SIGNAL.

FT	SIGNAL	1	28	NGF RECEPTOR.
FT	CHAIN	29	427	EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	29	250	POTENTIAL.
FT	TRANSMEM	251	272	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	273	427	4 X TNFR-CYS.
FT	DOMAIN	31	189	TNFR-CYS 1.
FT	REPEAT	31	65	TNFR-CYS 2.
FT	REPEAT	66	107	TNFR-CYS 3.
FT	REPEAT	108	147	TNFR-CYS 4.
FT	REPEAT	148	189	DEATH DOMAIN.
FT	DOMAIN	344	421	BY SIMILARITY.
FT	DISUFLID	32	43	BY SIMILARITY.
FT	DISUFLID	57	44	BY SIMILARITY.
FT	DISUFLID	44	64	BY SIMILARITY.
FT	DISUFLID	67	83	BY SIMILARITY.
FT	DISUFLID	86	99	BY SIMILARITY.
FT	DISUFLID	89	107	BY SIMILARITY.
FT	DISUFLID	109	122	BY SIMILARITY.
FT	DISUFLID	125	138	BY SIMILARITY.
FT	DISUFLID	128	146	BY SIMILARITY.
FT	DISUFLID	149	164	BY SIMILARITY.
FT	DISUFLID	167	180	BY SIMILARITY.
FT	DISUFLID	170	188	BY SIMILARITY.
FT	DOMAIN	197	248	SER/THR-RICH.
FT	CARBOHYD	60	80	POTENTIAL.
FT	SEQUENCE	427 AA;	45183 MW;	EE2924BD CRC32:

Query Match	7.0%;	Score 213;	DB 6;	Length 427;
Best Local Similarity	34.9%;	Pred. No. 1.15e-21;		
Matches	45;	Conservative	19;	Mismatches 60;
			Indels	5;
			Gaps	5;

Db 44 ckaenlgevaaprgan-tytcepcslsvtsdvstpeokpte-cvqigsmapcve 101
Qy 41 CDKCRPRGYLKQHTAKMKTYCACPDPHY-ytdsmhnsdecltycspvckelqyvkocnR 99
Db 102 addvvcayayuydettytceacrcvceagqlyfscgdkantvceecpqtysdeanhv 161
Qy 100 tHnrvceckberyl-Et-EfclKhrscprpgegvvaqactpranivckrkrpdpofsnetsk 157
Db 162 drclprctvc 170
Qy 158 APCRKHTNC 166

RESULT	14	STANDARD;	PRT;	425 AA.
ID	NGFR-RAT			
AC	P07174;			
RC	01-APR-1988 (REL. 07, CREATED)			
CC	01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)			
DE	01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)			
GN	LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)			
OS	(GP80-LINGR).			
OC	NGFR.			
CC	RATUUS NORVEGICUS (RAT).			
CC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
CC	EUTHERIA; RODENTIA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RL	MEDLINE; 87115859.			
RA	RADECK M.J., MISKO T.P., HSU C., HERZENBERG L.A., SHOOTER E.M.;			
RL	NATURE 325:593-597(1987).			
RN	[2]			
RP	SEQUENCE OF 1-22 FROM N.A.			
RC	TISSUE-LIVER.			
CC	MEDLINE; 93077038.			
RA	METSIS M., TIMMOSK T., ALLIKETS R., SAARMA M., PERSSON H.;			
RL	GENE 121:247-254(1992).			
CC	-1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,			
CC	NT-3, AND NT-4.			
CC	-1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE			
CC	BOND FORMATION.			
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	-1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.			

CC -1- SIMILARITY: CONSTRAINTS A LA-NGPR/TNFR-TYPE CYSTEINE-RICH REGION
DR EMBL: X05137; G56756; -
DR EMBL: X61269; -; NOT_ANNOTATED_CDS.
DR PIR: A26431; A26431.
DR HSP: P19438; 1TNFR.
DR PROSITE: PS00652; 1TNFR_NGPR.
DR PROSITE: PS0017; DEATH_DOMAIN.
DR REEFOR1; NEUROGENESIS; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT;
KM PHOSPHORYLATION; SIGNAL.

FT	CHAIN	30	425	NGF RECEPTOR.
FT	DOMAIN	30	251	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	252	273	POTENTIAL.
FT	DOMAIN	274	425	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	32	190	4 X TNFR-CYS.
FT	REPEAT	32	66	TNFR-CYS 1.
FT	REPEAT	67	108	TNFR-CYS 2.
FT	REPEAT	109	148	TNFR-CYS 3.
FT	REPEAT	149	190	TNFR-CYS 4.
FT	DOMAIN	198	249	SER/THR-RICH.
FT	DOMAIN	354	419	DEATH DOMAIN.
FT	DISULFID	33	44	BY SIMILARITY.
FT	DISULFID	45	58	BY SIMILARITY.
FT	DISULFID	48	65	BY SIMILARITY.
FT	DISULFID	68	84	BY SIMILARITY.
FT	DISULFID	87	100	BY SIMILARITY.
FT	DISULFID	90	108	BY SIMILARITY.
FT	DISULFID	110	123	BY SIMILARITY.
FT	DISULFID	126	139	BY SIMILARITY.
FT	DISULFID	129	147	BY SIMILARITY.
FT	DISULFID	150	165	BY SIMILARITY.
FT	DISULFID	168	181	BY SIMILARITY.
FT	DISULFID	171	189	BY SIMILARITY.
FT	CARBOHYD	61	61	POTENTIAL.
FT	CARBOHYD	71	71	POTENTIAL.
EQ	SEQUENCE	423 AA;	45432 MW;	7D78E258 CRC32;

Query Match	6.88;	Score 207;	DB 6;	Length 425;
Best Local Similarity	33.38;	Pred. No. 1.87e-20;		
Matches	43;	Conservative	21;	Mismatches 60; Indels 5; Gaps 4;

Db 45 kcaenlgsyqvapsgan-qtvccepclnlvtsdvastepkpcrte-clgysmsapcve 102
 QY 41 CDCPBPgYHlKQHCtAKKtVtCACPpHY-ITDSMHTSDECLYCSpCKEELQYKQCNr 99
 Db 103 addacvcrayyydeetghceaacsvceyglvfcscdkntycceespqetysdaanhv 162
 QY 100 THNRYCECKESRtYtEIE-FCLKRSRCPgGVVQAGtPERNtVCKKCPDGFfSNERSK 157
 Db 163 drcclpvc 171
 QY 158 APCRHtNC 166

RESULT	15			
ID	FASA_BOVIN	STANDARD;	PRT;	323 AA.
AC	p51867,			
DT	01-OCT-1996 (REL. 34, CREATED)			
DT	01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)			
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)			
DE	FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)			
DE	(APO-1 ANTIGEN) (CD95).			
GN	APT1 OR FAS			
OS	BOS Taurus (BOVINE).			
OC	EUDAROTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; ARTIODACTYLA.			
RN	[1]			
RN	SEQUENCE FROM N.A.			
RP	MEEDINE; 96226401.			
RA	YOO J., STONE R.T., BEATTIE C.W.;			
RL	DNA CELL BIOL. 15:227-234(1996).			
CC	-1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. MEDITES			
CC	CELL DEATH. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE			

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